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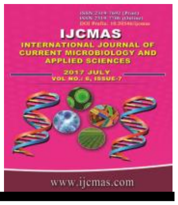

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# Study of Stability Analysis of Rice Varieties through Non- Parametric Approaches in Chhattisgarh, India

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## ABSTRACT

**Keywords**

ANOVA, GEI, Genotypes, Non parametric measures and Stability analysis.

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The promising rice varieties were grown in different agro-ecological regions of Chhattisgarh state to study their adaptability to varying climatic and soil conditions. Yield data collected from Department of Agriculture (CG) of 10 rice varieties at 10 locations during *kharif*-2011-12 to 2013-14. Result of the combined or pooled ANOVA revealed that varieties, environment and genotype-environment interaction were highly significant. Significant genotypic variance indicated genetic diversity among genotypes yield. Partitioning of the variance component indicated that 12.42 % due to varieties, 65.92 % due to varieties and locations, 18.31 % due to varieties and years, 3.14 % varieties x locations x years and 0.20 % due to error. Further the results of non-parametric stability analysis indicated that the stability value of Swarna (0.01), MTU-1010 (1.33) and IR-36 (1.33) rice varieties were found to be among the most stable varieties for both the methods among all varieties and MTU 1001 (4.66) and PKV-HMT (3.33) were found unstable and ranked tenth and ninth in its stability. Choice of variety for increased grain yield in rice would, therefore, be expected to change yield stability by increasing the values of mean absolute rank difference S (1) and variance S (2) nonparametric stability statistics.

## Introduction

The stable genotype has consistent phenotypic performance over environments. The resultant effect of genotype and environment may not be always independent. The stable genotypes can be identified by evaluating them over locations. This is subjected to pooled analysis over environments. Interpretation of genotype x environment interaction (GEI) can be aided by statistical modelling. Models can be linear formulations such as joint regression (Yates and Cochran (1938), Finlay and Wilkinson (1963), Eberhart and Russell (1966) modelling). Modelling GEI in MLTs (Multi-location trials) helps to determine phenotypic stability of genotypes.

This concept has been defined in different ways with increasing numbers of stability parameters (Gauch and Zobel, 1996). Genotype by environment interactions are important sources of variation in any crop, and the term *stability* is sometimes used to characterize a genotype, which shows a relatively constant yield, independent of changing environmental conditions. On the basis of this idea**,** genotypes with a minimal variance for yield across different environments are considered stable. This idea of stability may be considered as a biological or static concept of stability (Becker and Leon, 1988). This concept of stability is not acceptable to most breeders and agronomists, who prefer genotypes with high mean yields and the potential to respond to agronomic inputs or better environmental conditions (Becker, 1981).

The high yield performance of released varieties is one of the most important targets of breeders, which explains why they prefer a dynamic concept of stability (Becker and Leon, 1988).

The statistical techniques applied to this type of data can be as follows: linear formulations, like joint-regression (Yates and Cochran, 1938; Eberhart and Russell, 1966); multivariate clustering techniques (Lin and Butler, 1990); multiplicative methods based on additive main effects and multiplicative interaction (AMMI; Zobel *et al.*, 1988; Gauch, 1992); or nonparametric methods (Huehn, 1979). Genotype by environment interaction modeled using multi-environment trials can be used to assess phenotypic stability of genotypes, although phenotypic stability is often defined in a variety of ways, with increasing numbers of stability statistics having been developed (Gauch and Zobel, 1996; Sabaghnia *et al.*, 2006).

There are two major approaches to studying genotype by environment interactions and determining the adaptation of genotypes (Huehn, 1996). The most common approach is parametric analyses, which are based on statistical assumptions about the distribution of genotypic, environmental and GEI effects. Another approach is nonparametric or analytical clustering, which makes no specific modeling assumptions when relating environments and phenotypes relative to biotic and abiotic environmental factors.

Parametric measures of phenotypic stability are mostly related to variance components or related statistics. These stability estimates have good properties under certain statistical assumptions, based on the normal distribution of errors and interaction effects, but may not perform well if these assumptions are violated by factors such as the presence of outliners (Huehn, 1990a). Due to the fact that parametric tests for the significance of variances and variance related measures can be very sensitive to the underlying statistical assumptions an alternative approach is to use techniques such as non-parametric measures that are more robust to departures from the assumptions used in parametric analysis (Adugna and Labuschagne, 2003).

## Materials and Methods

Secondary yield data has been collected for rice from Department of Agriculture, Chhattisgarh state during three years (2011-12 to 2013-14). Description of promising varieties with duration and their characteristics *viz;* rice ten varieties as follows in table 1. Table 2 represents environmental effects such as; locations, temperature, rainfall (mm) and area (in ha.) of rice varieties respectively. Management and fertilization at each location were done according to cultural practices by farmer. Fertilization rates with planting were inflated with about 10% to ensure good and even stands and development.

## Conventional analysis of variances

The classic model for analysing the total yield variation contained in GEI observations is the analysis of variance (Fisher, 1918). The within-environment residual mean square measures the error in estimating the genotype means due to differences in soil fertility and other factors, such as shading and competition from one plot to another. After removing the replicate effect when combining the data, the GE observations are partitioned into two sources: (a) additive main effect for genotypes and environments and (b) non-additive effects due to GEI. The analysis of variance of the combined data expresses the observed ($Y_{ij}$) mean yield of the $i^{th}$ genotype at the $j^{th}$ environment as

$$Y_{ij} = \mu + G_i + E_j + GE_{ij} + e_{ij}$$

Where, μ is the general mean; $G_i$, $E_j$, and $GE_{ij}$ represent the effect of the genotype, environment, and the GEI, respectively; and $\varepsilon_{ij}$ is the average of the random errors associated with the $r^{th}$ plot that receives the $i^{th}$ genotype in the $j^{th}$ environment. The non-additive interaction as defined implies that the expected value of the $i^{th}$ genotype in the $j^{th}$ environment ($Y_{ij}$) depends not only on the levels of G and separately but also on the particular combination of levels of G and E (Crossa, 1990).

The stability measures were determined by the ANOVA analysis, the effects of the varieties, locations and years as well as their first and second order interactions. Varieties were assumed to be fixed, and years and locations effects random.

The ANOVA method for estimating variance components consists of equating mean squares to their expectations and solving the resulting set of simultaneous equations as shown in tables 3 and 4 and are based on the model provided by Allard (1960), which was developed by Comstock and Moll (1963) for the determination of interaction variance components.

Where, Y, L, G and R are the number of years, environment (locations), genotypes (varieties) and replications, respectively. The $\sigma_e^2$ and $\sigma_e^2$ are components of variance of error and genotypes respectively. Combinations of the subscript identify the components, for the interactions. MS1 to MS5 are the observed values of the various mean squares.

Where, MS1 to MS5 are the values of the appropriate mean squares as indicated in table 3; $r$, $l$, and $y$ are the numbers of replicates, locations, and years, respectively, in which the varieties were evaluated.

A combined analysis of variance procedure is the most common method used to identify the existence of GEI from replicated multi-location trials. If the GEI variance is found to be significant, one or more of the various methods for measuring the stability of genotypes can be used to identify the stable genotype(s). A wide range of methods is available for the analysis of GEI and can be broadly classified into four groups: the analysis of components of variance, stability analysis, multivariate methods and qualitative methods.

## Nassar and Huhn's mean absolute rank difference S (1) and variance S (2)

This non-parametric test is based on the ranks of the genotypes across locations. This gives equal weight to each location or environment. Genotypes with less change in rank are expected to be more stable.

The mean absolute rank difference S (1) estimates are all possible pair wise rank differences across locations for each genotype. The S (2) estimates are simply the variances of ranks for each genotype over environments (Nassar and Huhn, 1987; Huhn, 1990 a & b). For S (1), entries may be tested for significantly less or more stable than the average stability/instability. For the variance of ranks S (2), smaller estimates may indicate relative stability. Often, S (2) has less power for detecting stability than S (1).

The S (1) may lose power when genotypes are similar in their interactions with the environments. Usually S (1) is the preferred parameter because of its ease of computation; it's clear and relevant interpretation. Furthermore, an efficient test of significance is available.

Huhn (1990 a & b) and Nassar and Huhn (1987) proposed four non-parametric stability statistics that combine mean yield and stability. Four parameters based on yield ranks of genotypes in each environment are derived as follows:

### Mean rank difference

$$S(1) = \frac{2\sum_{j}^{m-1}\sum_{j=j+1}^{m}\left|r_{ij} - r_{ij'}\right|}{[m(m-1)]}$$

### Variance of rank

$$S(2) = \frac{\sum_{j=1}^{m}(r_{ij} - \bar{r}_{i.})^2}{(m-1)}$$

Where $S(1)$ = mean of the absolute differences among the classification $i^{th}$ cultivar in $j^{th}$ environment, $S(2)$ = variance of classification $i^{th}$ cultivar in $j^{th}$ environment, l = number of genotypes, $m$ = number of environments, $r_{ij}$ = the rank of the $i^{th}$ genotype in the $j^{th}$ environment and $\bar{r}_{i.}$ = the mean rank across all environments for the $i^{th}$ genotype. Significant test to S (1) and $S(2)$ was calculated with $\chi^2 = \Sigma Z^{m}{}_{i}$, m=1, 2 which E ($S_i{}^{m}$) and V ($S_i{}^{m}$) are mean and variance of Z respectively.

### Tests of significance

One of the most crucial points in developing new stability parameters must be the availability of efficient tests of significance; for testing the stability of a single genotype and; for testing stability comparisons between certain genotypes.

Nassar and Huhn's mean absolute rank represent plots portrayed by mean yield (q/ha) vs. S (1) and S (2) values. Mean S (1) and S (2) values and grand mean yield divide both figures into four sections; section 1 refers that varieties have high yield and small S (1) and S (2) values, section 2 signs that varieties possess high yield and large S (1) and S (2) values, section 3 presents that varieties exist with low yield and large S (1) and S (2) values, and section 4 exhibits that varieties are of low yield and small S (1) and S (2) values.

## Results and Discussion

### Analysis of variance and estimation of variances component for rice yield

The Analysis of variance (ANOVA) was calculated for ten promising rice varieties in Chhattisgarh. The ANOVA for yield of rice varieties are presented in table 5. The mean squares for locations, varieties, and locations x varieties were highly significant, indicating that the variety differed in their pattern of response relative to each other in the various locations of Chhattisgarh state. Partitioning of the variance component indicated that 12.42 % due to varieties, 65.92 % due to varieties and locations, 18.31 % due to varieties and years, 3.14 % varieties x locations x years and

0.20 % due to error (Table 6). The large contribution of variance due to varieties, GEI, varieties and years, indicates the significant influence of GEI in evaluation rice yield performance in Chhattisgarh state. Similarly, huge contribution of G x E interaction was also reported by Mohammadi *et al.*, (2013) in which they indicated that GEI accounted for larger proportion.

## Nassar and Huhn's mean absolute rank difference S (1) and variance of ranks S (2)

The results of non-parametric stability measures, S (1) and S (2), were based on values of the varieties across locations and equal weightage to each location was given. Varieties with less change in rank were considered to be more stable. The S (1) estimates were based on all possible pair wise rank differences, while S (2) were based on variance of ranks for each variety across environments. For the variance of ranks S (2), smaller values indicate relative stability. It was observed that stability value of Swarna (0.01), MTU-1010 (1.33) and IR-36 (1.33) rice varieties were found to be among the most stable varieties for both the methods among all varieties and MTU 1001 (4.66) and PKV-HMT (3.33) were found unstable and ranked tenth, ninth and eight in its stability (Table 7), respectively (Alberts, 2004).

The significance tests for S (1) and S (2) calculated values based on the ranks of adjusted data and added for varieties to obtain Z (Chi) values. It were observed that Z (1) value 59.97 is higher than the critical value of $\chi^2$ = 8.79, which indicated that there was significant differences in rank stability among ten rice varieties across locations (Table 7).

## Graphically presents GxE interaction of non-parametric analysis

This part deals with graphical presentation of G x E interaction pattern. This has been achieved with providing a new similarity measure for the principal coordinate analysis. Graphs have been obtained for GE interaction as well as yield response pattern from live data used for the study. The graphs have helped in identifying four groups which can be considered separately for indepth analysis (Thennarasu, 1995)

**Table.1** List of rice varieties used for Non-Parametric analysis

| S N. | Varieties | Duration | Characteristics |
|---|---|---|---|
| 1 | Swarna | 140-150 | Dwarf, medium-slender grain and high yielding capacity |
| 2 | MTU-1010 | 112-115 | Semi-dwarf, long-slender grain |
| 3 | MTU-1001 | 130-135 | Stout grain, Semi dwarf |
| 4 | IR-36 | 115-120 | Dwarf, long-slender grain, tolerances for gall midge, blast and blight |
| 5 | IR-64 | 115-120 | Dwarf, long-slender grain, tolerances for blight and blast |
| 6 | Mahamaya | 125-130 | Dwarf, stouts grain, drought resistance, used for *Poha* and *Murra*, |
| 7 | Karmamasuri | 125-130 | Semi-dwarf, medium-slender, gall midge resistance, Tolerance for blight, best for food consumption |
| 8 | Bamleswari | 130-135 | Resistance for blight disease, tolerance for brown spot |
| 9 | PKV HMT | 130-135 | Semi-dwarf and slender grain |
| 10 | BPT 5204 | 135-140 | Semi-dwarf, medium-slender grain, blight resistance (is called Samba masuri) |

**Table.2** Environments that were used in the study from 2011-12 to 2013-14 for varieties of rice

| SN. | Location | Latitudes | Longitude | Temp. | Rainfall (mm) | Area |
|---|---|---|---|---|---|---|
| 1 | Raigarh | 21.89 | 83.39 | 29°-49° | 1520 | 1 Ha. |
| 2 | Janjgir champa | 22.34 | 82.70 | 32°-47° | 1282 | 1 Ha. |
| 3 | Bilaspur | 22.07 | 82.13 | 23°-43° | 1229 | 1 Ha. |
| 4 | Raipur | 21.23 | 81.63 | 28°-47° | 1352 | 1 Ha. |
| 5 | Durg | 21.18 | 81.28 | 27°-45° | 1330 | 1 Ha. |
| 6 | Rajnandgaon | 21.09 | 81.03 | 30°-46° | 1505 | 1 Ha. |
| 7 | Mahasamund | 21.08 | 82.12 | 28°-43° | 1355 | 1 Ha. |
| 8 | Dhamtari | 20.71 | 81.55 | 28°-44° | 1436 | 1 Ha |
| 9 | Kanker | 20.27 | 81.49 | 20°-40° | 1591 | 1 Ha |
| 10 | Bastar | 19.08 | 82.02 | 19°-41° | 1540 | 1 Ha |

**Table.3** Form of variance analysis and mean square expectations for GEI

| Source | DF | MS | Expected mean square |
|---|---|---|---|
| Years (Y) | (Y-1) | | |
| Locations(L) | (L-1) | | |
| Y x L | (Y-1) (L-1) | | |
| Reps in Loc and Years | LY (R-1) | | |
| Genotypes (G) | (G-1) | MS5 | $\sigma_e^2 + r\sigma_{gly}^2 + rl\sigma_{gy}^2 + ry\sigma_{gl}^2 + rly\sigma_g^2$ |
| G x L | (G-1)(L-1) | MS4 | $\sigma_e^2 + r\sigma_{gly}^2 + ry\sigma_{gl}^2$ |
| G x Y | (G-1)(Y-1) | MS3 | $\sigma_e^2 + r\sigma_{gly}^2 + rl\sigma_{gy}^2$ |
| G x L x Y | (G-1)(L-1) (Y-1) | MS2 | $\sigma_e^2 + r\sigma_{gly}^2$ |
| Error | LY(G-1)(R-1) | MS1 | $\sigma_e^2$ |

**Table.4** Estimation of variance components and methods of determining GEI

| Variance component | Methods of Determination |
|---|---|
| Genotypes ($\sigma_g^2$) | (MS5+MS2-MS3-MS4) / *rly* |
| Genotypes x Location($\sigma_{gl}^2$) | (MS4-MS2) / *ry* |
| Genotypes x years ($\sigma_{gy}^2$) | (MS3-MS2) / *rl* |
| Genotypes x locations x years ($\sigma_{gly}^2$) | (MS2-MS1) / *r* |
| Error ($\sigma_e^2$) | MS1 |

**Table.5** Combined ANOVA for rice yield and the percentage sum of squares of the used environments over a period of three years 2011-12 to 2013-14

| Source | DF | SS | SS% | MS | F- value | P<0.01 |
|---|---|---|---|---|---|---|
| Years | 2 | 227.72 | 1.24 | 113.86 | 426.73 | ** |
| Locations | 9 | 897.79 | 4.91 | 99.75 | 373.86 | ** |
| Years x Locations | 18 | 500.84 | 2.74 | 27.82 | 104.28 | ** |
| Varieties | 9 | 9254.82 | 50.67 | 1028.31 | 3.85 | ** |
| Varieties x Years | 18 | 264.96 | 1.45 | 14.72 | 55.17 | ** |
| Varieties x Locations | 81 | 5510.77 | 30.17 | 68.03 | 254.98 | ** |
| Varieties x Years x Locations | 162 | 1524.85 | 8.35 | 9.41 | 35.27 | ** |
| Residual | 300 | 80.04 | 0.43 | 0.26 | | |
| **Total** | **599** | **18261.82** | | | | |

**Table.6** Estimation of variance components of rice promising varieties and Their interaction for grain yield

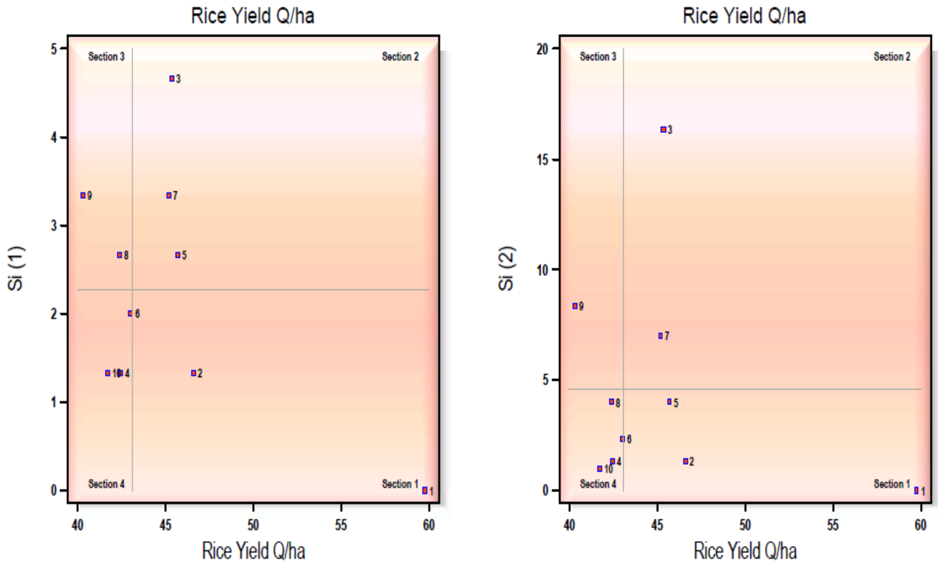
| Variance component | Method of Determination | |
|---|---|---|
| Varieties ($\sigma_g^2$) | 1.16 | 12.42 % |
| Varieties x Location($\sigma_{gl}^2$) | 6.16 | 65.92 % |
| Varieties x years ($\sigma_{gy}^2$) | 1.71 | 18.31 % |
| Varieties x locations x years ($\sigma_{gly}^2$) | 0.29 | 3.14 % |
| Error ($\sigma_e^2$) | 0.02 | 0.20 % |

**Table.7** Mean absolute rank difference S (1) and variance of ranks S (2) for rice varieties at across locations

| SN. | Varieties | Mean Yield (q/ha) | Rank | S(1) | Rank | Z(1) | S(2) | Rank | Z(2) |
|---|---|---|---|---|---|---|---|---|---|
| G1 | Swarna | 50.25 | 1 | 0.01 | 1 | 23.52 | 0.01 | 1 | 1.68 |
| G2 | MTU 1010 | 44.36 | 5 | 1.33 | 2 | 8.35 | 1.33 | 3 | 1.18 |
| G3 | MTU 1001 | 47.49 | 2 | 4.66 | 10 | 4.03 | 4.66 | 10 | 1.62 |
| G4 | IR 36 | 40.49 | 8 | 1.33 | 3 | 8.35 | 1.33 | 4 | 1.18 |
| G5 | IR 64 | 46.08 | 4 | 2.66 | 6 | 0.86 | 4.00 | 7 | 0.44 |
| G6 | Mahamaya | 46.34 | 3 | 2.00 | 5 | 3.65 | 2.33 | 5 | 0.86 |
| G7 | Karmamasuri | 43.41 | 6 | 3.33 | 8 | 1.00 | 7.00 | 8 | 0.03 |
| G8 | Bamleswari | 42.09 | 7 | 2.66 | 7 | 0.86 | 4.00 | 6 | 0.44 |
| G9 | PKV HMT | 36.79 | 10 | 3.33 | 9 | 1.00 | 3.33 | 9 | 0.00 |
| G10 | BPT 5204 | 38.45 | 9 | 1.33 | 4 | 8.35 | 1.00 | 2 | 1.30 |
| | Grand mean | 43.57 | | | | | | | |

Over all Chi-square for stability = 59.97, 10 df. Individual Z (1) distributed as single df. Chi-squares. Over all Chi-square for stability = 8.79, 10 df. Individual Z (2) distributed as single df. Chi-squares.

**Fig.1** Nassar and Huhn's S (1) and S (2) for mean yield of rice over Three years in different environments



It was observed from figure 1, mean values of varieties between two methods such as S (1) and S (2) divide both figures into four sections; section 1 shows that MTU-1010 (G2) and Swarna (G1) had high yield and small S (1) and S (2) values, section 2 shows that MTU-1001 (G3), Karmamasuri (G7) and IR-64 (G5) observed high yield and large S (1) and S (2) values, section 3 represents those varieties which exhibits low yield and large S (1) and S (2) values were Bamleswari (G8) and PKV-HMT (G9) and section 4 represents those varieties which showed low yield and small S (1) and S (2) values were IR-36 (G4) and BPT-5204 (G10). In our study, varieties in section 1 and 2 both can be considered as stable were MTU-1010 (G2) and Swarna (G1).

In conclusion, Non-parametric stability measurements seem to be useful alternatives to parametric measurements (Yue *et al.*, 1997), although they do not supply information about genotype adaptability. In fact, there are several reasons to prefer nonparametric stability models, one being that outlier bias is avoided and no assumptions are needed about the distribution of the data and the second is that nonparametric statistics are easy to use and to interpret. Based on these considerations, it appears that the estimation of stability is an appropriate approach for GEI analysis, this view being supported by the fact that a variety of parametric and nonparametric stability measures have been compared in the literature (Lin *et al.*, 1986; Flores *et al.*, 1998; Sabaghnia *et al.*, 2006). These statistics can be used by breeders and agronomists who need to make selection based upon genotype x environment interactions.

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